

RAW SEQUENCE LISTING

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Application Serial Number: 10/546,000
Source: PCT
Date Processed by STIC: 08/29/2005

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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/546,000

DATE: 08/29/2005

TIME: 18:10:22

Input Set : A:\Seqlist.txt
 Output Set: N:\CRF4\08292005\J546000.raw

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4 <110> APPLICANT: Hamada, Hirofumi
5   Ito, Yoshinori
6   Takahashi, Kazuhiro
7   Morikawa, Masayuki
9 <120> TITLE OF INVENTION: Methods For Treating Ischemic Diseases
12 <130> FILE REFERENCE: 50026/054001
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/546,000
C--> 14 <141> CURRENT FILING DATE: 2005-08-18
14 <150> PRIOR APPLICATION NUMBER: PCT/JP04/000957
15 <151> PRIOR FILING DATE: 2004-01-30
17 <150> PRIOR APPLICATION NUMBER: JP 2003-040806
18 <151> PRIOR FILING DATE: 2003-02-19
20 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3372
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)...(3372)
33 <400> SEQUENCE: 1
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35 Met Asp Ser Leu Ala Ser Leu Val Leu Cys Gly Val Ser Leu Leu Leu
36   1           5           10          15
38 tct gga act gtg gaa ggt gcc atg gac ttg atc ttg atc aat tcc cta      96
39 Ser Gly Thr Val Glu Gly Ala Met Asp Leu Ile Leu Ile Asn Ser Leu
40           20          25          30
42 cct ctt gta tct gat gct gaa aca tct ctc acc tgc att gcc tct ggg      144
43 Pro Leu Val Ser Asp Ala Glu Thr Ser Leu Thr Cys Ile Ala Ser Gly
44           35          40          45
46 tgg cgc ccc cat gag ccc atc acc ata gga agg gac ttt gaa gcc tta      192
47 Trp Arg Pro His Glu Pro Ile Thr Ile Gly Arg Asp Phe Glu Ala Leu
48           50          55          60
50 atg aac cag cac cag gat ccg ctg gaa gtt act caa gat gtg acc aga      240
51 Met Asn Gln His Gln Asp Pro Leu Glu Val Thr Gln Asp Val Thr Arg
52   65          70          75          80
54 gaa tgg gct aaa aaa gtt gtt tgg aag aga gaa aag gct agt aag atc      288
55 Glu Trp Ala Lys Lys Val Val Trp Lys Arg Glu Lys Ala Ser Lys Ile
56           85          90          95
58 aat ggt gct tat ttc tgt gaa ggg cga gtt cga gga gag gca atc agg      336
59 Asn Gly Ala Tyr Phe Cys Glu Gly Arg Val Arg Gly Glu Ala Ile Arg
60           100         105         110

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62	ata cga acc atg aag atg cgt caa caa gct tcc ttc cta cca gct act	384
63	Ile Arg Thr Met Lys Met Arg Gln Gln Ala Ser Phe Leu Pro Ala Thr	
64	115 120 125	
66	tta act atg act gtg gac aag gga gat aac gtg aac ata tct ttc aaa	432
67	Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys	
68	130 135 140	
70	aag gta ttg att aaa gaa gaa gat gca gtg att tac aaa aat ggt tcc	480
71	Lys Val Leu Ile Lys Glu Glu Asp Ala Val Ile Tyr Lys Asn Gly Ser	
72	145 150 155 160	
74	ttc atc cat tca gtg ccc cg ^g cat gaa gta cct gat att cta gaa gta	528
75	Phe Ile His Ser Val Pro Arg His Glu Val Pro Asp Ile Leu Glu Val	
76	165 170 175	
78	cac ctg cct cat gct cag ccc cag gat gct gga gtg tac tcg gcc agg	576
79	His Leu Pro His Ala Gln Pro Gln Asp Ala Gly Val Tyr Ser Ala Arg	
80	180 185 190	
82	tat ata gga gga aac ctc ttc acc tcg gcc ttc acc agg ctg ata gtc	624
83	Tyr Ile Gly Gly Asn Leu Phe Thr Ser Ala Phe Thr Arg Leu Ile Val	
84	195 200 205	
86	cgg aga tgt gaa gcc cag aag tgg gga cct gaa tgc aac cat ctc tgt	672
87	Arg Arg Cys Glu Ala Gln Lys Trp Gly Pro Glu Cys Asn His Leu Cys	
88	210 215 220	
90	act gct tgt atg aac aat ggt gtc tgc cat gaa gat act gga gaa tgc	720
91	Thr Ala Cys Met Asn Asn Gly Val Cys His Glu Asp Thr Gly Glu Cys	
92	225 230 235 240	
94	att tgc cct cct ggg ttt atg gga agg acg tgt gag aag gct tgt gaa	768
95	Ile Cys Pro Pro Gly Phe Met Gly Arg Thr Cys Glu Lys Ala Cys Glu	
96	245 250 255	
98	ctg cac acg ttt ggc aga act tgt aaa gaa agg tgc agt gga caa gag	816
99	Leu His Thr Phe Gly Arg Thr Cys Lys Glu Arg Cys Ser Gly Gln Glu	
100	260 265 270	
102	gga tgc aag tct tat gtg ttc tgt ctc cct gac ccc tat ggg tgt tcc	864
103	Gly Cys Lys Ser Tyr Val Phe Cys Leu Pro Asp Pro Tyr Gly Cys Ser	
104	275 280 285	
106	tgt gcc aca ggc tgg aag ggt ctg cag tgc aat gaa gca tgc cac cct	912
107	Cys Ala Thr Gly Trp Lys Gly Leu Gln Cys Asn Glu Ala Cys His Pro	
108	290 295 300	
110	ggt ttt tac ggg cca gat tgt aag ctt agg tgc agc tgc aac aat ggg	960
111	Gly Phe Tyr Gly Pro Asp Cys Lys Leu Arg Cys Ser Cys Asn Asn Gly	
112	305 310 315 320	
114	gag atg tgt gat cgc ttc caa gga tgt ctc tgc tct cca gga tgg cag	1008
115	Glu Met Cys Asp Arg Phe Gln Gly Cys Leu Cys Ser Pro Gly Trp Gln	
116	325 330 335	
118	ggg ctc cag tgt gag aga gaa ggc ata ccg agg atg acc cca aag ata	1056
119	Gly Leu Gln Cys Glu Arg Glu Gly Ile Pro Arg Met Thr Pro Lys Ile	
120	340 345 350	
122	gtg gat ttg cca gat cat ata gaa gta aac agt ggt aaa ttt aat ccc	1104
123	Val Asp Leu Pro Asp His Ile Glu Val Asn Ser Gly Lys Phe Asn Pro	
124	355 360 365	
126	att tgc aaa gct tct ggc tgg ccg cta cct act aat gaa gaa atg acc	1152

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127	Ile	Cys	Lys	Ala	Ser	Gly	Trp	Pro	Leu	Pro	Thr	Asn	Glu	Glu	Met	Thr	
128	370						375								380		
130	ctg	gtg	aag	ccg	gat	ggg	aca	gtg	ctc	cat	cca	aaa	gac	ttt	aac	cat	1200
131	Leu	Val	Lys	Pro	Asp	Gly	Thr	Val	Leu	His	Pro	Lys	Asp	Phe	Asn	His	
132	385						390				395				400		
134	acg	gat	cat	ttc	tca	gtt	gcc	ata	ttc	acc	atc	cac	cg	atc	ctc	ccc	1248
135	Thr	Asp	His	Phe	Ser	Val	Ala	Ile	Phe	Thr	Ile	His	Arg	Ile	Leu	Pro	
136							405			410				415			
138	cct	gac	tca	gga	gtt	tgg	gtc	tgc	agt	gtg	aac	aca	gtg	gct	ggg	atg	1296
139	Pro	Asp	Ser	Gly	Val	Trp	Val	Cys	Ser	Val	Asn	Thr	Val	Ala	Gly	Met	
140							420			425				430			
142	gtg	gaa	aag	ccc	ttc	aat	tct	gtt	aaa	gtt	ctt	cca	aag	ccc	ctg		1344
143	Val	Glu	Lys	Pro	Phe	Asn	Ile	Ser	Val	Lys	Val	Leu	Pro	Lys	Pro	Leu	
144							435			440				445			
146	aat	gcc	cca	aac	gtg	att	gac	act	gga	cat	aac	ttt	gct	gtc	atc	aac	1392
147	Asn	Ala	Pro	Asn	Val	Ile	Asp	Thr	Gly	His	Asn	Phe	Ala	Val	Ile	Asn	
148							450			455				460			
150	atc	agc	tct	gag	cct	tac	ttt	ggg	gat	gga	cca	atc	aaa	tcc	aag	aag	1440
151	Ile	Ser	Ser	Glu	Pro	Tyr	Phe	Gly	Asp	Gly	Pro	Ile	Lys	Ser	Lys	Lys	
152	465						470				475				480		
154	cct	cta	tac	aaa	ccc	gtt	aat	cac	tat	gag	gct	tgg	caa	cat	att	caa	1488
155	Leu	Leu	Tyr	Lys	Pro	Val	Asn	His	Tyr	Glu	Ala	Trp	Gln	His	Ile	Gln	
156							485			490				495			
158	gtg	aca	aat	gag	att	gtt	aca	ctc	aac	tat	ttg	gaa	cct	cg	aca	gaa	1536
159	Val	Thr	Asn	Glu	Ile	Val	Thr	Leu	Asn	Tyr	Leu	Glu	Pro	Arg	Thr	Glu	
160							500			505				510			
162	tat	gaa	ctc	tgt	gtg	caa	ctg	gtc	cgt	cgt	gga	gag	ggt	ggg	gaa	ggg	1584
163	Tyr	Glu	Leu	Cys	Val	Gln	Leu	Val	Arg	Arg	Gly	Glu	Gly	Glu	Gly		
164							515			520				525			
166	cat	cct	gga	cct	gtg	aga	cgc	ttc	aca	aca	gct	tct	atc	gga	ctc	cct	1632
167	His	Pro	Gly	Pro	Val	Arg	Arg	Phe	Thr	Thr	Ala	Ser	Ile	Gly	Leu	Pro	
168							530			535				540			
170	cct	cca	aga	ggt	cta	aat	ctc	ctg	cct	aaa	agt	cag	acc	act	cta	aat	1680
171	Pro	Pro	Arg	Gly	Leu	Asn	Leu	Leu	Pro	Lys	Ser	Gln	Thr	Thr	Leu	Asn	
172	545						550				555				560		
174	ttg	acc	tgg	caa	cca	ata	ttt	cca	agc	tcg	gaa	gat	gac	ttt	tat	gtt	1728
175	Leu	Thr	Trp	Gln	Pro	Ile	Phe	Pro	Ser	Ser	Glu	Asp	Asp	Phe	Tyr	Val	
176							565			570				575			
178	gaa	gtg	gag	aga	agg	tct	gtg	caa	aaa	agt	gat	cag	cag	aat	att	aaa	1776
179	Glu	Val	Glu	Arg	Arg	Ser	Val	Gln	Lys	Ser	Asp	Gln	Gln	Asn	Ile	Lys	
180							580			585				590			
182	gtt	cca	ggc	aac	ttg	act	tcg	gtg	cta	ctt	aac	aac	tta	cat	ccc	agg	1824
183	Val	Pro	Gly	Asn	Leu	Thr	Ser	Val	Leu	Leu	Asn	Asn	Leu	His	Pro	Arg	
184							595			600				605			
186	gag	cag	tac	gtg	gtc	cga	gct	aga	gtc	aac	acc	aag	gcc	cag	ggg	gaa	1872
187	Glu	Gln	Tyr	Val	Val	Arg	Ala	Arg	Val	Asn	Thr	Lys	Ala	Gln	Gly	Glu	
188							610			615				620			
190	tgg	agt	gaa	gat	ctc	act	gct	tgg	acc	ctt	agt	gac	att	ctt	cct	cct	1920
191	Trp	Ser	Glu	Asp	Leu	Thr	Ala	Trp	Thr	Leu	Ser	Asp	Ile	Leu	Pro	Pro	

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192	625	630	635	640	
194	caa cca gaa aac atc aag att tcc aac att aca cac tcc tcg gct gtg				1968
195	Gln Pro Glu Asn Ile Lys Ile Ser Asn Ile Thr His Ser Ser Ala Val				
196	645	650	655		
198	att tct tgg aca ata ttg gat ggc tat tct att tct tct att act atc				2016
199	Ile Ser Trp Thr Ile Leu Asp Gly Tyr Ser Ile Ser Ser Ile Thr Ile				
200	660	665	670		
202	cgt tac aag gtt caa ggc aag aat gaa gac cag cac gtt gat gtg aag				2064
203	Arg Tyr Lys Val Gln Gly Lys Asn Glu Asp Gln His Val Asp Val Lys				
204	675	680	685		
206	ata aag aat gcc acc atc att cag tat cag ctc aag ggc cta gag cct				2112
207	Ile Lys Asn Ala Thr Ile Ile Gln Tyr Gln Leu Lys Gly Leu Glu Pro				
208	690	695	700		
210	gaa aca gca tac cag gtg gac att ttt gca gag aac aac ata ggg tca				2160
211	Glu Thr Ala Tyr Gln Val Asp Ile Phe Ala Glu Asn Asn Ile Gly Ser				
212	705	710	715	720	
214	agc aac cca gcc ttt tct cat gaa ctg gtg acc ctc cca gaa tct caa				2208
215	Ser Asn Pro Ala Phe Ser His Glu Leu Val Thr Leu Pro Glu Ser Gln				
216	725	730	735		
218	gca cca gcg gac ctc gga ggg ggg aag atg ctg ctt ata gcc atc ctt				2256
219	Ala Pro Ala Asp Leu Gly Gly Lys Met Leu Leu Ile Ala Ile Leu				
220	740	745	750		
222	ggc tct gct gga atg acc tgc ctg act gtg ctg ttg gcc ttt ctg atc				2304
223	Gly Ser Ala Gly Met Thr Cys Leu Thr Val Leu Leu Ala Phe Leu Ile				
224	755	760	765		
226	ata ttg caa ttg aag agg gca aat gtg caa agg aga atg gcc caa gcc				2352
227	Ile Leu Gln Leu Lys Arg Ala Asn Val Gln Arg Arg Met Ala Gln Ala				
228	770	775	780		
230	tcc caa aac gtg agg gaa gaa cca gct gtg cag ttc aac tca ggg act				2400
231	Phe Gln Asn Val Arg Glu Glu Pro Ala Val Gln Phe Asn Ser Gly Thr				
232	785	790	795	800	
234	ctg gcc cta aac agg aag gtc aaa aac aac cca gat cct aca att tat				2448
235	Leu Ala Leu Asn Arg Lys Val Lys Asn Asn Pro Asp Pro Thr Ile Tyr				
236	805	810	815		
238	cca gtg ctt gac tgg aat gac atc aaa ttt caa gat gtg att ggg gag				2496
239	Pro Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu				
240	820	825	830		
242	ggc aat ttt ggc caa gtt ctt aag gcg cgc atc aag aag gat ggg tta				2544
243	Gly Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu				
244	835	840	845		
246	cgg atg gat gct gcc atc aaa aga atg aaa gaa tat gcc tcc aaa gat				2592
247	Arg Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp				
248	850	855	860		
250	gat cac agg gac ttt gca gga gaa ctg gaa gtt ctt tgt aaa ctt gga				2640
251	Asp His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly				
252	865	870	875	880	
254	cac cat cca aac atc atc aat ctc tta gga gca tgt gaa cat cga ggc				2688
255	His His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Glu His Arg Gly				
256	885	890	895		

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258 tac ttg tac ctg gcc att gag tac gcg ccc cat gga aac ctt ctg gac	2736
259 Tyr Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp	
260 900 905 910	
262 ttc ctt cgc aag agc cgt gtg ctg gag acg gac cca gca ttt gcc att	2784
263 Phe Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile	
264 915 920 925	
266 gcc aat agc acc gcg tcc aca ctg tcc tcc cag cag ctc ctt cac ttc	2832
267 Ala Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe	
268 930 935 940	
270 gct gcc gac gtg gcc cggtt ggc atg gac tac ttg agc caa aaa cag ttt	2880
271 Ala Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe	
272 945 950 955 960	
274 atc cac agg gat ctg gct gcc aga aac att tta gtt ggt gaa aac tat	2928
275 Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr	
276 965 970 975	
278 gtg gca aaa ata gca gat ttt gga ttg tcc cga ggt caa gag gtg tac	2976
279 Val Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr	
280 980 985 990	
282 gtg aaa aag aca atg gga agg ctc cca gtg cgc tgg atg gcc atc gag	3024
283 Val Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu	
284 995 1000 1005	
286 tca ctg aat tac agt gtg tac aca acc aac agt gat gta tgg tcc tat	3072
287 Ser Leu Asn Tyr Ser Val Tyr Thr Thr Asn Ser Asp Val Trp Ser Tyr	
288 1010 1015 1020	
290 ggt gtg tta cta tgg gag att gtt agc tta gga ggc aca ccc tac tgc	3120
291 Gly Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro Tyr Cys	
292 1025 1030 1035 1040	
294 ggg atg act tgt gca gaa ctc tac gag aag ctg ccc cag ggc tac aga	3168
295 Gly Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln Gly Tyr Arg	
296 1045 1050 1055	
298 ctg gag aag ccc ctg aac tgt gat gat gag gtg tat gat cta atg aga	3216
299 Leu Glu Lys Pro Leu Asn Cys Asp Asp Glu Val Tyr Asp Leu Met Arg	
300 1060 1065 1070	
302 caa tgc tgg cgg gag aag cct tat gag agg cca tca ttt gcc cag ata	3264
303 Gln Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro Ser Phe Ala Gln Ile	
304 1075 1080 1085	
306 ttg gtg tcc tta aac aga atg tta gag gag cga aag acc tac gtg aat	3312
307 Leu Val Ser Leu Asn Arg Met Leu Glu Glu Arg Lys Thr Tyr Val Asn	
308 1090 1095 1100	
310 acc acg ctt tat gag aag ttt act tat gca gga att gac tgt tct gct	3360
311 Thr Thr Leu Tyr Glu Lys Phe Thr Tyr Ala Gly Ile Asp Cys Ser Ala	
312 1105 1110 1115 1120	
314 gaa gaa gcg gcc	3372
315 Glu Glu Ala Ala	
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320 <211> LENGTH: 1124	
321 <212> TYPE: PRT	
322 <213> ORGANISM: Homo sapiens	
324 <400> SEQUENCE: 2	

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date